

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)
Subject: gi|457225 ref|NP_000005.1| alpha-2-macroglobulin precursor sp|P01023|A2MG_HUMAN ALPHA-2-MACROGLOBULIN
PRECURSOR (ALPHA-2-M) pir||MAHU alpha-2-macroglobulin precursor - human >gb|AAA51551.1| (M11313) alpha-2-macroglobulin
precursor [Homo sapiens] (SEQ ID NO: 23)
Length = 1474

Score = 2714 (960.4 bits), Expect = 1.7e-281, P = 1.7e-281
Identities = 596/1494 (39%), Positives = 874/1494 (58%)

Query: 13 LLLGMLALSPAIAEELPNYLVTLPARNFPSQVKVCLDSPGYSDVKFTVTLETCKDTQK 192
 LLL +L +++ + P Y+V +P+ L+ + +K C+ LS V + +LE+ +
Sbjct: 14 LLLVLLPTDASVSGK-PQYMLVLPVPSLLHTTETTEKGCVLVLYNETVTVSASLESVRGNRS 72

Query: 193 LLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFEEKKKVLIQRQNGTFV 372
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV
Sbjct: 73 LFTDLEAENDVLHCVAFAVPK-SSSNEEVMLTVQVKGPTEFKKRTTVMVKNEDSLTFV 131

Query: 373 QTDKPLYTPGQOVVFRIVTMDSNFVPVNDKYSMVELQDPNSNRIRIAQWLEVVPEQGIVDLS 552
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S
Sbjct: 132 QTDKSIYKPGQTVKFRVWSMDENFHLNELIPLVYIQDPKGNRIAQWQSFQLEGGLKQFS 191

Query: 553 FQLAPEAMLGTYTVAAVE---GKTFFGTFVVEEVLPKFKVEVVEPKELSTVQESFLVKIC 723
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C
Sbjct: 192 FPLSSEPFQGSYKVVVQKSGGRTEHPFTVEEFLPKFEVQVTPVKIITILEEEMNVSVC 251

Query: 724 CRYTYGKPMLGAVQVSVQCANTYWYREVEREQLPDKCRNLSGQTDKTCGFSAPVDMATF 903
 YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F
Sbjct: 252 GLTYTGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCERKPSGQLNSHGCFYQQVKTKVF 309

Query: 904 DLIGYAYSHQINIVATVVEEGTGVVEANATQNIYISPMGSMFTFEDTSNFIHPNFPFSGKI 1083
 L Y +++ A + EEGT VE Q+ I+ + ++F + + PF G++
Sbjct: 310 QLKREYEMKLHTEAQIQEEGTVVVELTGRQSSBITRTITKLSFVKVDSHFPRQGIPIFFGQV 369

Query: 1084 RVRGHDDSLKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLETSGWNGTDVSLGKFQM 1263
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
Sbjct: 370 RLVDGKGVPINPKVIF--IRGNEANYYSNATTDHGLVQFSINTTNVMGTSLTVRVNYKD 427

Query: 1264 EDLVNPEQVPVRYQNAYLHLRPFYSTRSFLGHLRLNGPLKCGQPQEVLDVYIDPADA 1443
 Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Sbjct: 428 RSPCYGYQWVSEEHBAHTAYLVFSPKSFVHLEPMSHELPCGHTQTQVAHYILNGGTL 487

Fig 1A

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

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Query: 1444 SPDQEIFSYYLIGKGLVMEQKHLNSKKKGLKASFSLSLTFTSRLAPDPSLVIYAIFF 1623
      +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKKLSFYLLIMAKGGIVRTGTHGLLVKQEDMKGHFSIPVKSDIAPVARLLIYAVLP 547

Query: 1624 SGGVADKIQFSVGMCFDNQVSLGFSQSPQQLPGAELQQAAPGSLCALRAVDSEVLLL 1803
      +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCCLANKVDLSFSPSQSPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWFDPQLIDPMPQGHSSQRSIIW 1983
      +PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSSASSVYNLLP-----EKDLTGFPGPLN-DQDDEDCINRHNVIYINGITY 655

Query: 1984 RP-SFSEGTLFSFFRDVGLKILSNKIKKPVDCSH-----RSPE-----YSTAMGGG 2124
      P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSTNEKDMYSFLEDMLKAPTNSKIRKPKMCPQLQYEMHGPGLRVGFYEDVMGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITWKA MFC 2304
      GH P H VR+YFPETW+WDL + ++G V VTVPD ITEWKA +FC
Sbjct: 716 GHARLVHVEEP-HT---ETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDITTEWKAGAF 771

Query: 2305 TSQSRGFLSPTVGLTAFKPPFFVDLTLPYSVVRGESFRLTAFIFNYLKDCIRVQTDLAKS 2484
      S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLIGISSTASLRAFPFPFFVELTMPYSVIRGEAFTLKATVNLNLPKCIRVSVQLEAS 831

Query: 2485 HEYQLESWADSQTSCLCADDKTHHWNITAVKLGHNFTISTKILDSNEPCGGQKGFVP 2664
      + Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAF LAVPVEKEQAPHCICANGRQTVSWAVTPKSLGNVNFVSAEALAESQELCGTEVPSPV 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGKVASSESVSLLELPVDIVPDS TKAYTVTL 2844
      + GR DT+IKP+LV+PEG+ E T +SLLCP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVSEELSLKLPNNVVEESARASVSVL 951

Query: 2845 GKQLEILDSEKRRRMEAAKVVWRDIMGTAQNLDGLVQMPSGCGEQNMVLFAPIIYVLQYL 3024
      G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYGCGEQNMVLFAPNIYVLDYL 990

Query: 3025 EKAGLLTPEIRSRVAGFLEIGYQKELMYKHSNGSYSAFGERDGN--GNTWLTAFVTKCFG 3198
      + LT E++S+A+G+L GYQ++L YKH +GSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEVKS KAIGYLNLTGYQRQLNYKHYDGSYSTFGERYGRNQGNLTWLTAFVLKTFA 1050

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Fig. 1B

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

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Query: 3199 QAQKFIIDPKNIQDALKWMAGNQLPSGCYANVGNLLHTAMKGGVDDDEVSLTAYVTAALL 3378
      QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAYIFIDEAHITQALIWLSQRQKDNCGFRSSGLLNNAIKGVEDEVTL SAYITIAL 1110

Query: 3379 EMGKDVDPMVVSQGLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T ++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EIPLTVTHPVVRNALFCLE-SAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVLKS 1169

Query: 3538 LDQQAIIISGESIYWSQKPTPSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L+++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKKDINSVHWERPQKPKAPVGHFYEPAQPSAEVEMTSYVLLAYLTAQPAPTSEDLT 1229

Query: 3709 KATSIVAWLAKQHNAYGGSSTQDTVVVALQALAKY-ATTAYMPSEINLVVKSTENFQRT 3885
      AT+IV W+ KO NA GGSSTQDTVVVAL AL+KY A T + +S+ F
Sbjct: 1230 SATNIWKITKQNAQGGSSTQDTVVVALHALSKYGAATFRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFQODTLPNVPGMYTLEASGQGCVVQTVLRYNLPPTNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GCY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLLOQVSLPELPGEYSMKVTGEGCVLQTSKYNILPEKEEFPFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSYVGSRSSNMAIVEVKMLSGFSPMEGTNQLLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRASNNMAIVDKMVSGFIPKPTVKMLERSNHVSRTE 1409

Query: 4246 FGTDTLNIYLDLIKNTQTFTTISQSVLVTNLKPAATIKVYDYILPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVYDY F +++Y
Sbjct: 1410 VSSNHVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYETDEFAIAEY 1463

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FIG. 1C

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)
Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. (SEQ ID NO 24)
Length = 1474

Score = 2699 (955.2 bits), Expect = 3.2e-280, P = 3.2e-280
Identities = 596/1494 (39%), Positives = 870/1494 (58%)

Query: 13 LLLGMLALSPAIAEELPNYLVTLPARLNFPSPQVKVCLDLSPGYSVKFTVTLETYKDKTQK 192
Sbjct: LLL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +
Query: 13 LLLLVLPPTDASVSGKPQYMLVLPVSLLTETTEKGCVLLSYLNETVTVSASLESVRGNRS 72
Sbjct: L L L L L V L P T D A S V S G K P Q Y M L V L P V S L L T E T T E K G C V L L S Y L N E T V T V S A S L E S V R G N R S
Query: 193 LLEYSGLKKRHLHCISFLVPPPPAGTTEEVATIRVSGVNNISFEEKKKVLIIQRCNGTFV 372
Sbjct: L + LHC++F VP + EEV + V G F+++ V+++ + + FV
Query: 73 LFTDLEAENDVLHCVAFAVPK-SSSNEEVMFLTVQVKGPTQEFKKRTVMVKNEDSLV 131
Sbjct: L F T D L E A E N D V L H C V A F A V P K - S S S N E E V M F L T V Q V K G P T Q E F K K R T V M V K N E D S L V
Query: 373 QTDKPLYTPGQOVYFRIVTMDSNFVNDKYSMVLELQDPNSNRIAQWLEVVPEQIVDLS 552
Sbjct: QTDK +Y PGQ V FR+V+MD NF P+N+ +V +ODP NRIAOW E G+ S
Query: 132 QTDKSIYKPGQTVKFRVVSMDENFHLNELIPLVIYIQDPKGNRIQWQSFQLEGGLKQFS 191
Sbjct: Q T D K S I Y K P G Q T V K F R V V S M D E N F H L N E L I P L V I Y I Q D P K G N R I A Q W Q S F Q L E G G L K Q F S
Query: 553 FOLAPEAMLGYTVTVAE---GKTGTFVSEVEYVLPKPKVEVVEPKELSTVQESFLVKIC 723
Sbjct: F L + E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C
Query: 192 FPLSSEPFQGSYKVVVQKSGGRTEHPFTVEEFVLPKFEVQVTVPKIITILEEEMNV SVC 251
Sbjct: F P L S S E P F Q G S Y K V V V Q K S G G R T E H P F T V E E F V L P K F E V Q V T V P K I I T I L E E E M N V S V C
Query: 724 CRYTYGKPMGLAVQSVQCANTYWYREVEREQLPDKCRNLSGQTDKTCGCFAPVDMATF 903
Sbjct: YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F
Query: 252 GLYTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCFKFSGQLNSHGCFYQQVKTVP 309
Sbjct: G L Y T Y G K P V P G H V T V S I C R K Y S D A - - S D C H G E D S Q A F C F K F S G Q L N S H G C F Y Q Q V K T V P
Query: 904 DLIGAYSHQINIVATVVEEGTGVEANATQNIYISPMGSMTFEDTSNFYHPNFPFSGKI 1083
Sbjct: L Y +++ A + EEGT VE Q+ I+ + ++F + + PF G++
Query: 310 QLKRKEYEMKLHTEAQIQEEGTVELTGRQSSSEITRTITKLSFVKVDSHFRQGIPIFFGQV 369
Sbjct: Q L K R K E Y E M K L H T E A Q I Q E E G T V E L T G R Q S S S E I T R T I T K L S F V K V D S H F R Q G I P I F F G Q V
Query: 1084 RVRGHDDSF LKNHLVFLVIYGTNGTTFNQTLVTDNNGLAPFTLETSGMNGTVDVSLGKFQM 1263
Sbjct: R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
Query: 370 RLVDGKGVPINPKVIF--IRGNEANYYSNATDEHGLVQFSINTTNVMGTSLTVRVNYKD 427
Sbjct: Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Query: 1264 EDLVNPEQVPYRYQNAYLHLRPFYSTTRSLGIHRLNGLPKCGQPQEVLDVVDYIDPADA 1443
Sbjct: Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Query: 428 RSPCYGYQWVSEHEEAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTQVQAHVILNGGTL 487
Sbjct: R S P C Y G Y Q W V S E H E E A H T A Y L V F S P S K S F V H L E P M S H E L P C G H T Q T V Q A H V I L N G G T L
Query: 1444 SPDQETSFYYLICKGLVMEGQKHLNKKKGLKASFSLSLTFTSRLAPDPSLVIYAI 1623
Sbjct: +++SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Query: 488 LGLKKLSFYLLIMAKGGIVRTGTHGLLVQEDMKGHFISISIPVKSDIAPVARLLIYAVLP 547
Sbjct: L G L K K L S F Y L L I M A K G G I V R T G T H G L L V Q E D M K G H F I S I S I P V K S D I A P V A R L L I Y A V L P

Fig. 2A

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query: 1624 SGGVADKIQFSVGMCFDNOVSLGFSFSPQQLPGAELQLQAAPGSLCALRAVDSEVLL 1803
+G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENCCLANKVDLSFSPQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1804 RPDRELSNRSVYGMFFFWYGHYPYQVAEYDQCPVSGPWDFPQPLIDPMPQGHSSQRSIIW 1983
+PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPAELSSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 1984 RP-SFSEGTDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGGG 2124
P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSTNEKDMYSFLEDMGLKAFNSKIRKPKMCPQLQQYEMHGPGLRVGFYESDVMGR 715

Query: 2125 GHPEAFESSTPLHQAEDSQVRQYFPETWLDLFPIGNSGKEAVHVTVPDAITEWKAMSFC 2304
GH P H VR+YF ETW+WDL + ++G V VTPVD ITEWKA +FC
Sbjct: 716 GHARLVHVEEP-HT--ETVRKYFAETWIWDLVVNSAGVAEVGVTPDITITWKAGAFC 771

Query: 2305 TSQSRGFLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATIFNYLKDCIRVQTDLAKE 2484
S+ G G+S T L AF+PEFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S
Sbjct: 772 LSEDAGLGISSASTASLRAFQPFVVELTMPYSVIRGEAFTLKATLVNLYLPKIRVSVQLEAS 831

Query: 2485 HEYQLESWADSQTSCLCADDKAKTHWNITAVKLGHNFTISTKILDSNEPCGGQGFVP 2664
+ Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP
Sbjct: 832 PAFLAVPVEKEQAPHCICANGRQTVSAVTPKSLGNVNF+TVSAELESQELCGTEVPSPV 891

Query: 2665 QKGRSDTLIKPVLVKEGVLVEKTHSSLLCPKGVASESVSLELPVDIVPDSKAYVTVL 2844
+ GR DT+IKP+LV+PEG+ E T +SLCP G SE +SL+LP ++V +S +A V+VL
Sbjct: 892 EHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVSELSKLPNNVVEESARASVSVL 951

Query: 2845 GKQLEILLDSERKRRMEAAKVVWRDIMGTLQNLQDGLVQMPSGCGEQNMVLFAPIIYVLQYL 3024
G DI+G+A+QN L+QMP GCGEQNMVLFAP IYVL YL
Sbjct: 952 G-----DILGSAMQNTQNLQMPYGCGEQNMVLFAPNIYVLDYL 990

Query: 3025 EKAGILLTEEIRSAVGFLGIGYQKELMYKHSNGSYSAFGERDGN--GNTWLTAFVTKCFG 3198
+ LT EI+S+A+G+L GYQ++L YKH +GSYS FGER G GNTWLTAFV K F
Sbjct: 991 NETQQLTPEIKSKAIGYLNLTGQRLNYKHVDGSYSTFGERYGRNQNTWLTAFVLTFFA 1050

Query: 3199 QAQKFIFIDPKNIQDALKWMAGNQLPSGCYANVGNLLHTAMKGGVDDDEVSLTAVVTAALL 3378
QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGV+DEV+L+AY+T ALL
Sbjct: 1051 QARAVIFIDEAHITQALIWLSQRQKDNCGCFRSSGSLNNAIKGGVEDEVTL SAYITIAL 1110

Fig. 2B

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query: 3379 EMGKDVPMSVQGLRCLKNSATST-----TNLYTQALLAYIFSLAGEMDIRNILLKQ 3537
      E+ V P+V L CL+ SA T +++YT+ALLAY F+LAG D R +LK
Sbjct: 1111 EILLTVTHPVVRNALFCLE-SAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKREVLKS 1169

Query: 3538 LDQQAIIISGESIYWSQKPTPSSNASPWSEPA--VDVELTAYALLAQLT-KPSLTQKEIA 3708
      L++++A+ S++W + P + + EP A +VE+T+Y LLA LT +P+ T +++
Sbjct: 1170 LNEEAVKKNDSVHWERPQPKAPVGHFYEPQAPSAEVEMTSYVLLAYLTAQPAPTSDDL 1229

Query: 3709 KATSIVAWLAKQHNA YGGFSSSTQDTVVVALQALAKY-AFTAYMPSEINLVVKSTENFQRT 3885
      AT+IV W+ KQ NA GGFSSSTQ TVVAL AL+KY A T + + ++S+ F
Sbjct: 1230 SATNIVKWIWKQNAQGGFSSSTQHTVVVALHALSKYGAATFTRTGKAAQVTIQSSGTFSSK 1289

Query: 3886 FNIQSVNRLVFQDDTLPNVPGMYTLEASGGCVVYQTVLRYNLPPTNNMKTFSLSVEIGK 4065
      F + + NRL+ QQ +LP +PG Y+++ +G+GCVY+QT L+YNILP F+L V+
Sbjct: 1290 FQVDNNRLLQQVSLPELPGEYSMKVTGCGCVYLTQSLKYNILPEKEEFPFALGVQTL 1349

Query: 4066 ARCEQPTSPRSLTLTIHTSVYGSRSSNNMAIVEVKMLSGFSPMEGTNQLLLQQPLVKKVE 4245
      C++P + S +++ SY GSR+SNMAIV+VKM+SGF P++ T ++L + V + E
Sbjct: 1350 QTCDEPKAHTSFQISLSVSYTGSRSSASNMAIVDKVMVSGFIPLKPTVKMLERSNHVSRTE 1409

Query: 4246 FGTDTLNIYLDLIKNTQTYTFTISQSVLVTNLKPATIKVYDY YLPGSFKLSQY 4407
      ++ + IYLD++ T + FT+ Q V V +LKPA +KVVDY F +++Y
Sbjct: 1410 VSSNHVLIYLDKRVSNQTL SLFTVLTQDVPVRDLKPAIVKVYDY YETDEFAIAEY 1463

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FIG. 2C

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
OVOS_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)
Subject: >sp|P20740|OVOS_CHICK OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) >pir||A20872 ovostatin precursor - chicken
>emb|CAA55384.1| (X78801) ovomacroglobulin, ovostatin [Gallus gallus] (SEQ ID NO: 41)
Length = 1473

Score = 1300 (462.7 bits), Expect = 6.1e-135, Sum P(2) = 6.1e-135
Identities = 297/849 (34%), Positives = 457/849 (53%), Frame = +3

Query: 96 VYKFPVSPTRKMAQALLGLMLALSPAIAEEL-PNYLVTLPARLNFPPSVQKVCLDLSPGYS 272
+ F ++ KMW + +L +L L A +E P Y++ +PA L S +VCL
Sbjct: 9 ILSFFCLTVRKMWLKFILAILLLHAAAGKEPEPQYVLMVPAVLQSDSPSQVCLQFFNLNQ 68

Query: 273 DVKFTVTLETQDKTKLLEYSGLKRRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFE 452
+ V LE + E + L C++F++PP + +A I + G +
Sbjct: 69 TISVRVVLEYDTINTTIFEKNTTNSGLQCLNFMIPPVT--SVSLAFISFTAKGTTFDLK 126

Query: 453 EKKKVLIIQRQNGTFVQTDKPLYTPGQQVYFRIVTMDSNFVPNDKYSMVLELQDPNSNRI 632
E++ V+I + FVQTDKP+Y PGQ V FR+V +D NF PV + Y ++ +QDP +NRI
Sbjct: 127 ERRSVMINWMESEFVQTDKPIYKPGQSVMFVRVALDFNFKPQVQEMYPLIAVQDPQNNRI 186

Query: 633 AQMLEVVPEQGIVDLSPQLAPEAMLGTYTVAAE--G-KTFGTFSEVEEYVLPKFKVEVVE 803
QW V E IV + F L E +LG Y + V + G +T +F VEEVLPKF V V
Sbjct: 187 FQWQNVTSSEINIVQIEFPLTEEPILGNKYIIVTKKSGERTSHSFLVEEYVLPKFDVTVTA 246

Query: 804 PKELSTVQESFLVKICCRYTYGKPMGLGAVQVSVQKANTVWYREVEREQLPDKCRNLSGQ 983
P L+ + VKIC YTYG+P+ G VQ+SVQ+ ++Y R + C++ +
Sbjct: 247 PGSLTVMDSSELTWKICAVITYGQPVVEGKVQLSVCRDFDSYG-----RCKKSPVCQSFTKD 301

Query: 984 TDKTGCFSAPVDMATFDLIGYAYSHQINIVATVVEEGTGV EANATQNIYISPMGSMTFE 1163
D GC S + F+L Y +++ A V E+ ATQ+I I+ M S+ FE
Sbjct: 302 LDTDGCLSHILSSKVFELNRIGRYKRNLDVKAIVTEKEQVCNLTATQISITQVMSSSQFE 361

Query: 1164 DTSNPHYHPNFPFSGKIRVRGHDDSF LKNHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLET 1343
+ + Y P+ G+I++ D+S + N ++ L + N T N T TD NG+APF+++T
Sbjct: 362 NVDDHYRRGIPYFGQIKLVKDKNSPISKVQLFVNKN-TNFT--TDINGIAPFSIDT 418

Fig 3A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
OVOS_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

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Query: 1344 SGWNGTDVSLGKFKQMEDLVYNPEQVPRVYQNAVYHLRPFYSTTRSLGIHRLNGLKCG 1523
      S ++SL+ ++ D ++ + Y +A L ++ YS T SF+ I L + CG
Sbjct: 419 SKIFPELSLKALYKTSQCHSEGWIEPSYPDASLSVQRLYSWTSSVRIEPLWKDMSCG 478

Query: 1524 PQEVLVDYYIDPADASPDQEIYSFSYYLIGKSLVMEQKHLNSKKKGLKASFSLSLTFT 1703
      Q + + V Y ++ ++F Y + KG +V+ G+ +N + +F + L
Sbjct: 479 QKRMITVYYILNTEGYEHINIVFYVGMAGKIVLTGEIKVNIQADQ-NGTFMIFLVVN 537

Query: 1704 SRLAPDPSLVIYAIFFPSGGVVADKIQFSVEMCFDNQVSLGFSQQLPGAELQLQAAP 1883
      ++AP L++Y + P+ +VAD ++FS+E CF N+V L FS Q L + V L ++AA
Sbjct: 538 EKMAPALRLLVNMLHPAKELVADSVRFSEKCFKKNVQLQFSEKQMLTTSNVSLVIEAAA 597

Query: 1884 GSLCALRAVDESLLLLRPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWDFPQPL 2063
      S CA+RAVD+S+LLL+ + ELS ++Y + P Q ++ + D PQ
Sbjct: 598 NSFCAVRAVDKSMMLLKSETLSAETIYNLHPI-----QDLQGYIFNGLNLE--DDPQ-- 648

Query: 2064 IDPMFQGHSS-QRSIIWRPFSFSE-GTDLFSFPRDVGLKILSNAKIKKPVDCSH---RSPE 2228
      DP + + +RP S G D++ F RD+G+K +N+KI++P C+ R P
Sbjct: 649 -DPCVSSDDIFHKGLYRPLTSGGLPDPVYQFLRDMGMKFFFTNSKIRQTVCTREIVRPPS 707

Query: 2229 YSTAMG--AGGGHPE-----AFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGEAVH 2387
      Y G A H + A E H E +R++FPETW+WD+ I ++GK +V
Sbjct: 708 YFLNAGFTASTHVVKLSAEVAREERGRHILET--IREFFPETWIWDILINSTGKASVS 765

Query: 2388 VTVPDAITEWKAMSFCTSQSRGFGLSPTVGLTAFKPPFFVDLTLPYSVVRGESFRLTATIF 2567
      T+PD ITEWKA +FC + GFG+S LTAF+PPFFVDLTLPYS++ GE F + A +F
Sbjct: 766 YTIPDITIEWKASAFCEELAGFGMSVPAITLTAFAFPFFVDLTLPYSIIHGDFLVRANVF 825

Query: 2568 NYLKD CIRV 2594
      NYL CI++
Sbjct: 826 NYLNHC IKI 834

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Fig 3B

BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)
Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. SEQ ID NO: 24
Length = 1474

Score = 1289 (458.8 bits), Expect = 5.6e-134, Sum P(2) = 5.6e-134
Identities = 300/834 (35%), Positives = 448/834 (53%), Frame = +3

Query: 141 LLLGMLALSPAIAEELPNYLVTLPARLNFPSPQKVCLDSPGYSDVKFTVTLETKDKTQK 320
 LLL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +
Sbjct: 13 LLLLVLPVDASVSGKPQYMLVPSLLHTTEKGCVLVSLNETVTVSASLESVRGNRS 72

Query: 321 LLEYSGLKKRHLHCISFLVPPPPAGGTEEVATIRVSGVGNNISFEKKKKVLIQRQNGTFV 500
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV
Sbjct: 73 LFTDLEAENDVLHCVAFAVPK-SSSNEEVNFLTQVKGPTQEFKKRTTVMVKNEDSLVPV 131

Query: 501 QTDKPLYTPGQQVYFRIVTMDSNFVPVNDKYSMVELQDPNSNRIAQWLEVVPEQGIVDLS 680
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAQW E G+ S
Sbjct: 132 QTDKSIYKPGQTVKFRVVSMDENFHLPLVIYIQDPKGNRIAQWQSFQLEGGKQFS 191

Query: 681 FQLAPEAMLGTVTVAE---GKTFGTFSVEEYVLPKFKVEWEPKELSTVQESFLVKIC 851
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C
Sbjct: 192 FPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFEVQVTPVKIITILEEEMNVSVC 251

Query: 852 CRYTYGKPMLGAVQSVQCQKANTYWYREVEREQLPDKCRNLSGQTDKTCGCFSAFVDMATF 1031
 YTYGKP+ G V VS+C+K + + E C SGQ + GCF V F
Sbjct: 252 GLTYGKPVPGHVTVSICRKYSDA--SDCHGEDSQAFCCKFSGQLNSHGCFYQQVTKTVF 309

Query: 1032 DLIGAYASHQINIVATVVEGTGVEANATQNIYISPGMSMTFEDTSNPHYHPNPFPSGKI 1211
 L Y +++ A + EGT VE Q+ I+ + ++F + + + PF G++
Sbjct: 310 QLKRKEYEMKHLTEAQIQEETGVVELTGRQSSEITRTITKLSFKVKVDSHFRQGIPIFGQV 369

Query: 1212 RVRGHDDSFLLKNHLVFLVIYGTNGTFTNQTLVTDNNGLAPFTLETSGWNGTQDVSLGKPFQM 1391
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++
Sbjct: 370 RLVDGKGVPIPNKVIF--IRGNEANYSNATTDHGLVQFSINTTNVMGTSLTVRVNYKD 427

Query: 1392 EDLVNPEQVPRIYQNAVYHLRPFYSTTSFLGIHRLNGPLKCGQPQEVLDVYIDPADA 1571
 Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++
Sbjct: 428 RSPCYGYQWVSEEEHAAHTAYLVFSPSKSFVHLEPMSHELPCGHTQTQVAHYILNGGTL 487

Fig. 4A

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH
RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

Query: 1572 SPDQEIFSYLLIGKSLVMEGQKHLNSKKGLKASFSLSLTFTSR LAPDPFSLVIYAI 1751
+---SF Y ++ KG +V G L K++ +K FS+S+ S +AP L+IYA+ P
Sbjct: 488 LGLKLSFYLLIMAKGGIVRTGTHGLLVKQEDMKGHFSISIPVKSDIAPVARLLIYAVLP 547

Query: 1752 SGGVVADKIQFSVEMCFDNQVSLGFSQSPSQQLPGAELVQLQAAPGSLCALRAVD 1931
+G V+ D ++ VE C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+
Sbjct: 548 TGDVIGDSAKYDVENC LANKVDLSFSPSQSLPASHAHLRVTAAPQSVCALRAVDQSVLLM 607

Query: 1932 RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWDFPQPPLIDPMPQGHSSQ 2111
+PD ELS SVY + P E D GP + Q D + + + I +
Sbjct: 608 KPDAELSASSVYNLLP-----EKDLTGFPGLN-DQDDEDCINRHNVIYINGITY 655

Query: 2112 RP-SFSEGTDLFSFFFRDVG LKILSNAKIKKPVDCSH-----RSPE-----YSTAMGAG 2252
P S + D++SF D+GLK +N+KI+KP C PE Y + + G
Sbjct: 656 TPVSSTNEKDMYSFLEDMGLKAFNTSKIRKPKMCPQLQQYEMHGPGLRVGFYESDV-MG 714

Query: 2253 GGHPEAFESSTPLHQAEDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITEWKAMSF 2432
GH P H VR+YF ETW+WDL + ++G V VTVPD ITEWKA +F
Sbjct: 715 RGHARLVHVEEP-HT---ETVRKYFAETWIWDLVVVNSAGVAEVGVTVPDITTEWKAGAF 770

Query: 2433 CTSQSRGFLSPTVGLTAFKPFVVDLTLPYSVVRGESFRLTATIFNYLKD CIRV 2594
C S+ G G+S T L AF+PFV+LT+PYSV+RGE+F L AT+ NYL CIRV
Sbjct: 771 CLSE DAGLGISS T ASLRAFQPFVVELTMPYSVIRGEAFTLKATVNLNYPKCIRV 824

Fig. 4B